Exhibit A (handwritten)

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:            May 7, 2004, 21:29:10 ; Search time 29.5753 Seconds
                   (without alignments)
                   1109.503 Million cell updates/sec

Title:             US-09-961-400-2
Perfect score:     578
Sequence:          1 QDWLTFQKKHLTNTRDVDCN..........TFCVTCENQAPVHFVGVGHC 104

Scoring table:     BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched:          1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters:   1017041

Post-processing:   Minimum Match 0%
                   Maximum Match 100%
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :         SPTREMBL_25:*
                   1:  sp_archea:*
                   2:  sp_bacteria:*
                   3:  sp_fungi:*
                   4:  sp_human:*
                   5:  sp_invertebrate:*
                   6:  sp_mammal:*
                   7:  sp_mhc:*
                   8:  sp_organelle:*
                   9:  sp_phage:*
                  10:  sp_plant:*
                  11:  sp_rodent:*
                  12:  sp_virus:*
                  13:  sp_vertebrate:*
                  14:  sp_unclassified:*
                  15:  sp_rvirus:*
                  16:  sp_bacteriap:*
                  17:  sp_archeap:*

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	DB ID	Description
1	578	100.0	127	13	Q918V8	q918v8 rana pipien
2	556	96.2	127	13	Q8UVX5	q8uvx5 rana pipien
3	404.5	70.0	129	13	Q9DFY6	q9dfy6 rana catesb
4	386	66.8	128	13	Q9DFY8	q9dfy8 rana catesb
5	311	53.8	128	13	Q9DFY7	q9dfy7 rana catesb
6	309	53.5	128	13	Q9DFY5	q9dfy5 rana catesb
7	298	51.6	133	13	Q98SM0	q98sm0 rana catesb
8	286	49.5	133	13	Q98SL9	q98sl9 rana catesb
9	285	49.3	132	13	Q98SM0	q98sm0 rana catesb
10	282	48.8	133	13	Q98SM2	q98sm2 rana catesb
11	280	48.4	132	13	Q98SL8	q98sl8 rana catesb
12	275.5	47.7	132	13	Q98SM1	q98sm1 rana catesb
13	157.5	27.2	169	13	Q9DF78	q9df78 rana catesb
14	157.5	27.2	146	6	Q9W738	q9w738 xenopus lae
15	129.5	22.4	146	6	Q861Y3	q861y3 pygathrix r
16	129.5	22.4	146	6	Q861Y2	q861y2 pygathrix b
17	129.5	22.4	146	6	Q861Y1	q861y1 pygathrix a
18		22.3	152	11	Q9JKI5	q9jki5 mus saxicol
18		22.0	157	11	Q9JKI9	q9jki9 meriones un
20		21.9	153	11	Q9JKI7	q9jki7 mus saxicol
21		21.8	157	11	Q9JKJ3	q9jkj3 meriones un
21		21.7	146	6	Q861Y4	q861y4 trachypithe
22		21.6	157	11	Q9JKJ4	q9jkj4 meriones un
23		21.3	154	11	Q9JKI8	q9jki8 mus saxicol
24		21.1	157	11	Q9JKJ1	q9jkj1 meriones un
25		20.9	147	6	Q7YRJ6	q7yrj6 balaena mys
26		20.9	157	11	Q9JKJ2	q9jkj2 meriones un
27		20.8	155	11	Q9JKI6	q9jki6 mus saxicol
28		20.7	155	11	Q9JKH9	q9jkh9 mus pahari
29		20.4	157	11	Q9JKJ3	q9jkj3 meriones un
30		20.2	155	11	Q9JKI3	q9jki3 mus saxicol
31		20.2	155	11	Q9JKI6	q9jki6 mus saxicol
32		20.0	132	6	Q9TV25	q9tv25 eulemur ful
33		20.0	155	11	Q9JKI2	q9jki2 mus saxicol
34		19.9	155	11	Q9JKI4	q9jki4 mus saxicol
35		19.8	146	6	Q861Y5	q861y5 colobus gue
36		19.6	155	11	Q9BC1	q9bc1 tragulus ja
37		19.6	119	6	Q9TV32	q9tv32 cercopithec
38		19.6	132	6	Q9TSQ6	q9tsq6 colobus gue
39		19.6	119	6	Q9TV24	q9tv24 gorilla gor
40		19.6	147	6	Q8HZQ0	q8hzq0 galago moho
41		19.6	155	11	Q9R134	q9r134 rattus norv
42		19.6	156	11	Q9JKG6	q9jkg6 mus musculu
43		19.6	155	11	Q9JKH7	q9jkh7 mus caroli
43		19.5	119	6	Q9TV30	q9tv30 saguinus oe
44		19.5	155	11	Q9R125	q9r125 mus musculu
45		19.5	155	11	Q9JKH8	q9jkh8 mus pahari

```
RESULT 1
ID   Q918V8
AC   Q918V8;                     PRELIMINARY;      PRT;    127 AA.
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Onconase variant rapLR1 precursor.
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20330357; PubMed=10871370;
RA   Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT   "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT   3' UTR of unusual length and structure.";
RL   Nucleic Acids Res. 28:2375-2382(2000).
DR   EMBL; AF165133; AAF76935.1; -.
DR   PIR; A39035; A39035.
DR   HSSP; P22069; 1ONC.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL          1       23
FT   SEQUENCE        127 AA;  14491 MW;  B851DC5407AB69B CRC64;
SQ
                          POTENTIAL.
```

ALIGNMENTS

```
Query Match       100.0%;
Best Local Similarity   100.0%;
Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Score 578;  DB 13;  Length 127;
Pred. No. 3.5e-59;
```

```
Qy     1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
```

```
Db    24  QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 83
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    61  SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
          ||||||||||||||||||||||||||||||||||||||||||||
Db    84  SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127
```

RESULT 2
Q8TUX5
```
ID   Q8TUX5      PRELIMINARY;   PRT;   127 AA.
AC   Q8TUX5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Onconase precursor.
GN   RPR.
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liao Y.-D., Wang S.-C.;
RT   "Rana pipiens onconase genomic DNA.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF332139; AAL54383.1; -.
DR   PIR; A39035; A39035.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNase_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL
SQ   SEQUENCE   127 AA;   14469 MW;   953F90D351CFEBF3 CRC64;

Query Match            96.2%;   Score 556;   DB 13;   Length 127;
Best Local Similarity  96.2%;   Pred. No. 1.2e-56;
Matches  100;   Conservative  2;   Mismatches  2;   Indels  0;   Gaps  0;

Qy    1  QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
Db   24  QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 83

Qy   61  SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
Db   84  SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 127
```

RESULT 3
Q9DFY6
```
ID   Q9DFY6      PRELIMINARY;   PRT;   129 AA.
AC   Q9DFY6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase4 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
```

```
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR   PDB; 1KVZ; 28-JUL-02.
DR   EMBL; AF242555; AAG31441.2; -.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23     POTENTIAL.
FT   CHAIN        24    129     RC-RNASE4 RIBONUCLEASE.
SQ   SEQUENCE   129 AA;   14724 MW;   826A62882B10ABDA CRC64;

Query Match            70.0%;   Score 404.5;   DB 13;   Length 129;
Best Local Similarity  67.6%;   Pred. No. 4.6e-39;
Matches  71;   Conservative  16;   Mismatches  17;   Indels  1;   Gaps  1;

Qy    1  QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
Db   24  QDWATFKKKHLITDTMDVDCDNLMPTSLFDCKDKNTFIYSLPGPVKALCRGVIFSADVLSN 83

Qy   61  SEFYLSDCNVTSR-PCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
Db   84  SEFYLAECNVKPRPKPCKYKLKKSSNRICIRCEHELPVHFAGVGHC 128
```

RESULT 4
Q9DFY8
```
ID   Q9DFY8      PRELIMINARY;   PRT;   128 AA.
AC   Q9DFY8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase2 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
```

```
DR   PDB; 1M58; 09-JAN-03.
DR   EMBL; AF242553; AAG31439.1; -.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23     POTENTIAL.
FT   CHAIN        24    128     RC-RNASE2 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;   14839 MW;   989719CF52053BCC CRC64;

Query Match            66.8%;   Score 386;   DB 13;   Length 128;
Best Local Similarity  67.3%;   Pred. No. 6.4e-37;
Matches  70;   Conservative  10;   Mismatches  24;   Indels  0;   Gaps  0;

Qy    1  QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
```